



Blast 2 Sequences

WARNING: First sequence must be nucleotide for this program

WARNING: Second sequence must be nucleotide for this program

Program Matrix

Match: Mismatch:

Open gap and extension gap penalties

gap x_dropoff expect word size ☒ Filter

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
TVNTPKMPKPNFQQFTGDDSPFCQEGSPFQSSPFCQGGQGGNGGGQQQAFMALGSGVILDAD
KGYVVTNNHVVDNATVIKVLSDGRKFDKAMVGKDPKSDIALIQIQNPKNLTAIKMADSDA
LRVGDTVAIGNPFLGETVTSGIVSALGRSGLNAENYENFIQTDAAINRGNSGGALVNLN
GELIGINTAILAPDGGNIGIGFAIPSNMVKNLTSQMVEYGVQVKGELGIMGTELNSELAKA
MKVDAQRGAFVSQVLPNSSAAKAGIKAGDVITSLNGKPISSFAALRAQVGTMPVGSKLTLG
LLRDGKQVNVNLELQQSSQNVQDSSSIFNGIEGAEMSNGKGDQGVVNVNVKTGTPAAQIGL
KKGDEVIIGANQQAVKNIAELRKVLDSKPSVLALNIQRGDSTIYLLMQ
```

DEG P y E. coli:

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
qsegpavvniqaapaprtqngsgnaetasapiadsapiyerrkrivpnmpaipqeeaaagg
lnfgsgfiiskngyiltntnhvvagmsikvllndkreytakligsdvqsdvallkidee
lpvkvignpknlpkgewaaigapfgfdnsvtagivsakgrslpnesytpfiqtdvainpg
nsggplfnlkgqvvnginsqiysrsggfmgisfaipidvamvnaeqlkntgkvqrgqlgvii
qevsyglagsfgldkasgaliakipgsaeraglgagdivlsldggeirssgdipvmvgai
tpgkevslgvwrkgeeitikaklgnaahtgassktdeapyeqqsgtfsvesagitlqth
tdssgkhlvvrvsdaaeraglrhgdeilavrsprq
```

SEQ ID NO: 4
6
091333, 098

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



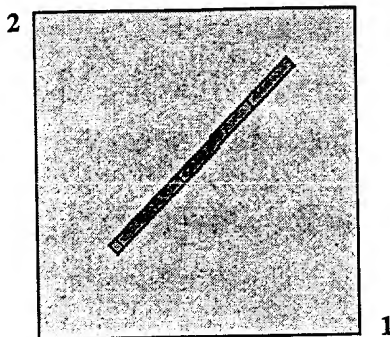
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** ☒ Filter

Sequence 1 lcl|seq_1 Length 474 (1..474)

Sequence 2 lcl|seq_2 Length 463 (1..463)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 217 bits (552), Expect = 3e-55
 Identities = 115/267 (43%), Positives = 177/267 (66%), Gaps = 3/267 (1%)

```

Query: 114 GSGVIIDADKGYVVTNNHVVDNATVIKVQLSDGRKFDAKMGKDPKSDIALIQIQNPKNL 173
          GSG II + GY++TN HVV IKV L+D R++ AK++G D +SD+AL++I + L
Sbjct: 126 GSGFIISKN-GYILTNTNTHVVGMSIKVLLNDKREYTAKLIGSDVQSDVALLKIDATEEL 184

Query: 174 TAIKMA DSDALRVGDYTV AIGNPFGLGETVTSGIVSALGRSGLNAENYENFIQTDAAINR 233
          +K+ + L+ G++ AIG PFG +VT+GIVSA GRS L E+Y FIQTD AIN
Sbjct: 185 PVVKIGNPKNLKPGEWVAAIGAPFGF DNSVTAGIVSAKGRS-LPNESYTPFIQTDVAINP 243

Query: 234 GNSGGALVNLNGELIGINTAILAPDGGNIGIGFAIPSNMVKNLTSQMVEYGQVKRGELGI 293
          GNSGG L NL G+++GIN+ I + GG +GI FAIP ++ N+ Q+ G+V+RG+LG+
Sbjct: 244 GNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQLGV 303

Query: 294 MGTELNSELAKAMKVDAQRGAFVSQVLPNSSAAKAGIKAGDVITSLNGKPISSFAALRAQ 353
          + E++ LA++ +D GA ++++ P S A +AG++AGD++ SL+G I S L
Sbjct: 304 IIQEVSYGLAQSFGLDKASGALIAKI-PGSPAERAGLQAGDIVLSLDGGEIRSSGDL PVM 362

Query: 354 VGTMPVGSKLTLGLLRDGKQVNVNLEL 380
          VG + G +++LG+ R G+++ + +L
Sbjct: 363 VGAITPGKEVSLGVWRKGEEITIKAKL 389
  
```

DEOP

seq. id. num. 09/388, 092

CPU time: 0.13 user secs. 0.02 sys. secs 0.15 total secs.

Gapped
 Lambda K H
 0.315 0.134 0.367

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 1763
Number of Sequences: 0
Number of extensions: 158
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 2
length of query: 474
length of database: 242,984,850
effective HSP length: 124
effective length of query: 350
effective length of database: 179,419,226
effective search space: 62796729100
effective search space used: 62796729100
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (22.0 bits)
S2: 73 (32.7 bits)